Amendment to the Claims:

Claim 1. (Currently amended) A method for producing ~~an~~ evolved microorganisms having an evolved methionine biosynthesis pathway for the biosynthesis of methionine by the metabolism of a simple carbon source and methylmercaptan as a source of sulfur, comprising:
a) generating a ~~directed modification in a gene of interest~~ modified microorganism by inactivating, deleting, or inhibiting expression of the *met*E gene in an initial microorganism, wherein the ability of said modified microorganism to grow is impaired when grown on a minimal medium containing no methionine, S-adenosylmethionine, homocysteine or cystathionine ~~to yield a modified microorganism wherein the production or consumption of a substrate is inhibited when the modified microorganism is grown on a defined medium, impairing the ability of the modified organism to grow;~~;
b) culturing ~~the~~ said modified microorganism obtained in step (a) on said ~~defined~~ minimal medium~~,~~ in the presence of methylmercaptan under selection pressure thereby allowing ~~the~~ said modified microorganism to evolve ~~a compensatory metabolic pathway~~ through a methionine biosynthesis pathway to compensate for ~~the~~ impaired growth ~~wherein the defined medium can contain a co-substrate promoting the evolution~~; and
c) selecting an evolved microorganism from step (b) able to grow on said ~~defined~~ minimal medium~~; wherein a compensatory metabolic pathway evolved allowing the microorganism to proliferate on the defined medium~~ in the presence of methylmercptan,
wherein the methionine biosynthesis pathway evolves such that methionine is produced by the metabolism of a simple carbon source and methylmercaptan as a source of sulfur thereby allowing said evolved microorganism to proliferate on said minimal medium containing no methionine, S-adenosylmethionine, homocysteine or cystathionine.

Claims 2-7 (cancelled)

Claim 8. (Currently amended) The method as claimed in claim 1, wherein ~~the~~ said evolved microorganism possesses at least one evolved gene coding for an evolved protein~~, the evolution~~

~~of which allows the inhibited growth to be compensated by the evolved metabolic pathway~~ involved in the methionine biosynthesis pathway.

Claim 9. (Currently Amended) The method as claimed in claim 8, comprising ~~wherein it includes~~ a step d) ~~consisting of~~ comprising the isolation of ~~the~~ said evolved gene coding for ~~the~~ an evolved protein involved in the methionine biosynthesis pathway.

Claim 10. (Cancelled)

Claim 11. (Previously presented) The method as claimed in claim 9, wherein the evolved gene is introduced, into a production microorganism intended for the production of the evolved protein.

Claims 12 - 25. (Cancelled)

Claim 26. (Currently Amended) The method of claim 1, wherein ~~the genetic modification comprises the~~ said inactivating, deleting, or inhibiting expression of the *met*E gene is performed by directed mutation of ~~a gene or deletion of a gene of interest~~ said *met*E gene~~,~~ or directed modification of ~~a~~ the promoter ~~in said gene of interest~~ of said *met*E gene.

Claim 27. (Currently Amended) The method of claim 1, wherein the ~~genetic modification~~ deletion of the *met*E gene ~~consists in the~~ includes removal of ~~the gene of interest~~ most of said *met*E gene.

Claim 28. (Currently Amended) The method of claim 1, wherein ~~the gene of interest~~ said *met*E gene is replaced with a selection marker gene.

Claim 29. (Currently Amended) The method of claim 1, wherein ~~the~~ said evolved microorganism is ~~selected among bacteria, yeasts and fungi~~ a bacteria.

Claim 30. (Currently Amended) The method of claim 1 ~~29~~, wherein ~~the~~ said evolved microorganism is ~~Aspergillus sp., Bacillus sp., Brevibacterium sp., Clostridium sp., Corynebacterium sp.,~~ an Escherichia sp.~~, Gluconobacter sp., Pseudomonas sp., Rhodococcus sp., Saccharomyces sp., Streptomyces sp., Xanthomonas sp., or Candida sp.~~

Claim 31. (Currently Amended) The method of claim 1 ~~29~~, wherein the microorganism is E. coli ~~and C. glutamicum~~.

Claim 32. (Currently Amended) An evolved ~~modified~~ microorganism having an evolved methionine biosynthesis pathway ~~made~~ produced by the method of claim 1.

Claim 33. (New) The method of claim 8, wherein said gene coding for an evolved protein involved in the methionine biosynthesis pathway is a mutated *met*B gene with methionine synthase activity which allows for the direct conversion of O-succinyl-L-homoserine into L-methionine with methylmercaptan as a sulfur source.

Claim 34. (New) The method of claim 9, wherein said gene coding for an evolved protein involved in the methionine biosynthesis pathway is a mutated *met*B gene with methionine synthase activity which allows for the direct conversion of O-succinyl-L-homoserine into L-methionine with methylmercaptan as a sulfur source.

Claim 35. (New) A method for the preparation of evolved strains of *E. coli* having an evolved methionine biosynthesis pathway for the biosynthesis of methionine by the metabolism of a simple carbon source and methylmercaptan as a source of sulfur, comprising:
(a) generating a modified microorganism by inactivating, deleting, or inhibiting expression of the *met*E gene in an initial *E. coli* strain, wherein the ability of said modified microorganism to grow is impaired when grown on a minimal medium containing no methionine, S-adenosylmethionine, homocysteine or cystathionine,
b) culturing said modified microorganism obtained in step (a) on said minimal medium in the presence of methylmercaptan under selection pressure thereby allowing said modified

microorganism to evolve through the methionine biosynthesis pathway to compensate for the impaired growth; and

c) selecting an evolved *E. coli* strain from step (b) able to grow on said minimal medium in the presence of methylmercptan, said evolved microorganism comprising a mutated *met*B gene with methionine synthase activity and allowing the direct conversion of O-succinyl-L-homoserine into L-methionine with methylmercaptan as a sulfur source.

Claim 36. (New) The method of claim 35, wherein said deletion includes the removal of most of said *met*E gene.

Claim 37. (New) The method of claim 35, wherein said *met*E gene is replaced with a selection marker gene.

Claim 38. (New) The method of claim 35, wherein said initial *E. coli* strain is strain *E. coli* K12.

Claim 39. (New) The method of claim 35, wherein said evolved *E. coli* strain is strain *E. coli* 183 deposited at the Collection Nationale de Cultures de Microorganisms (CNCM) and registered under the number I-3005.

Claim 40. (New) The method of claim 1, wherein said simple carbon source is selected from the group consisting of glucose, galactose, sucrose, lactose and molasses.